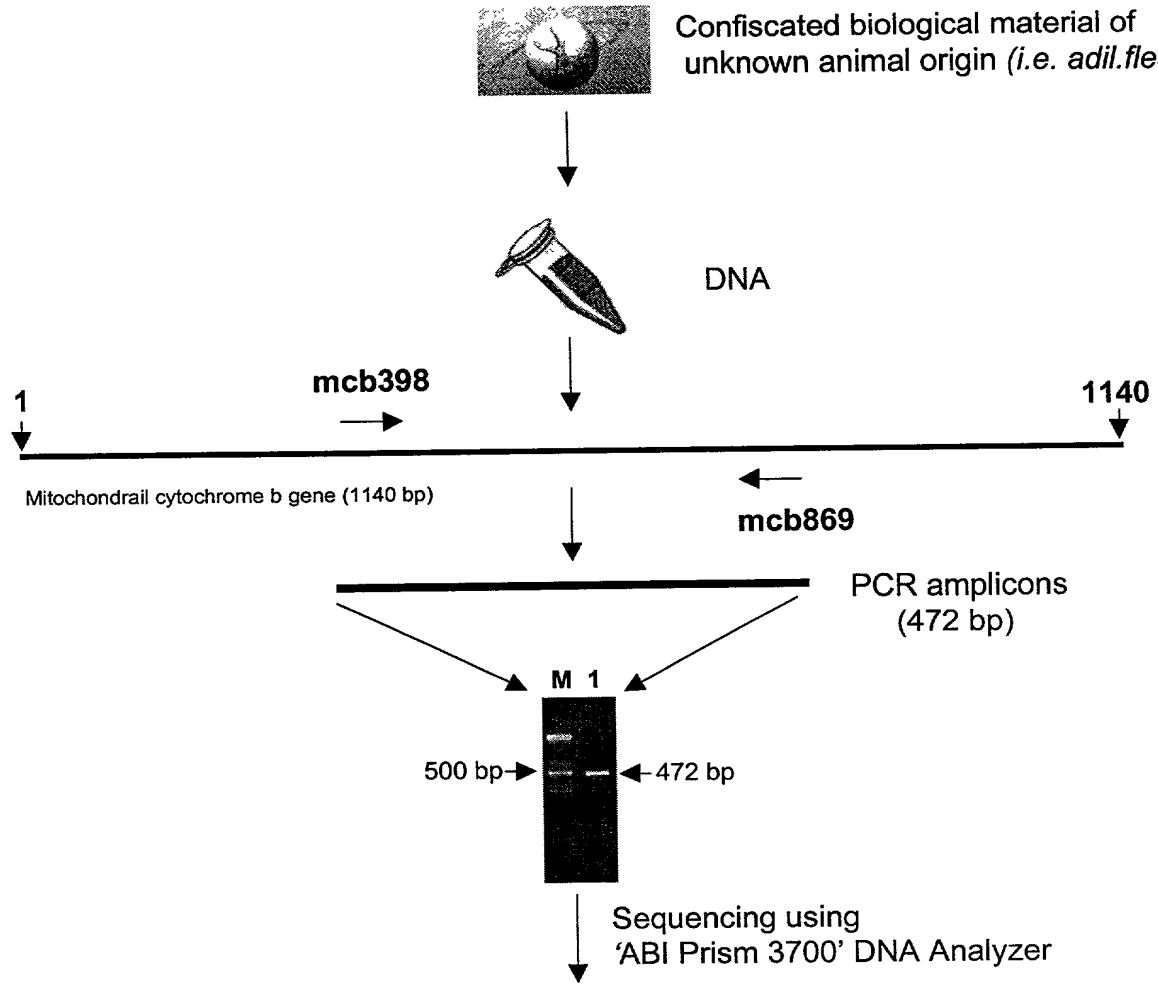
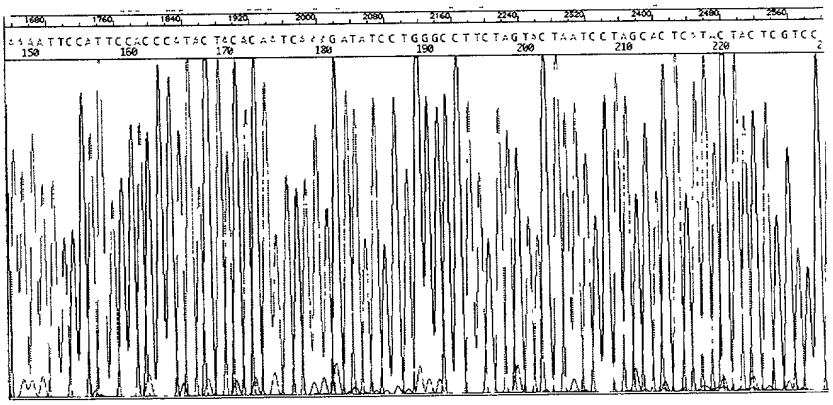




Revealed sequence (328 bp)

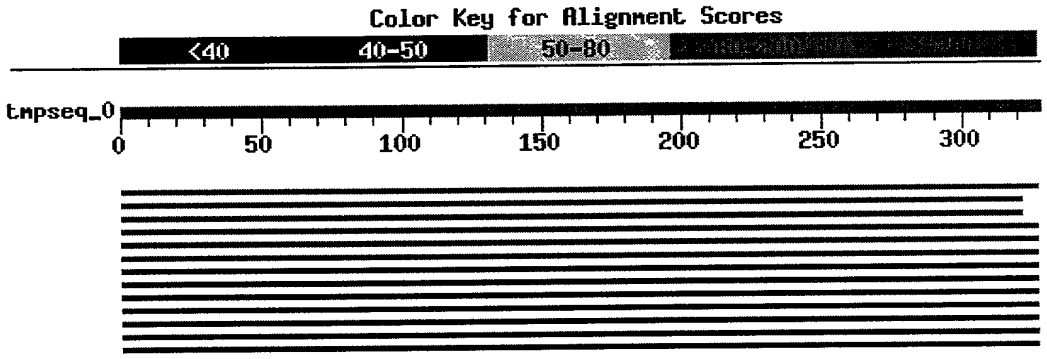
TGAATCTGAGGAGGCTTCTCAGTAGACAAAGCTACCCTGACAC
GATTCTTTGCCTTCCACTTCATCCTTCCATTTATCATCTCAGC
TCTAGCAGCAGTCCACCTCCTATTCCTTCACGAGACAGGATCT
AACAACCCCTCAGGAATAGTATCCGACTCAGACAAAATTCCAT
TCCACCCATACTACACAATCAAAGATATCCTGGGCCTTCTAGT
ACTAATCCTAGCACTCATACTACTCGTCCTATTCTCACCAGAC
CTGTTAGGAGACCCCGATAACTACATCCCTGCCAACCCTCTAA
ATACCCCTCCCCATATCAAGCCTGAAT

Figure 1 a

Sequence of cytochrome b gene (328 bp) revealed from biological material of unknown origin i.e. *'adil.flesh'* using primers **'mcb398'** and **'mcb869'**

↓ Homology search in *'nr'* database using *'BLAST'*

http://www.ncbi.nlm.nih.gov/BLAST/



Sequences producing significant alignments:	Score (bits)	E Value
gb|AY005809.1| ***Panthera pardus*** cytochrome b gene, partial c...	603	e-170
gb|AF053054.1|AF053054 *Panthera tigris sumatrae* isolate Su1...	527	e-147
gb|AF053053.1|AF053053 *Panthera tigris tigris* isolate B7 mi...	527	e-147
gb|AF053050.1|AF053050 *Panthera tigris corbetti* isolate C2 ...	476	e-132
gb|AF053049.1|AF053049 *Panthera tigris corbetti* isolate C1 ...	476	e-132

↓

Selection of reference animals based on above information and further analysis using primers **'mcb398'** and **'mcb869'**

↓ Multiple sequence alignments using *'Autoassembler'*

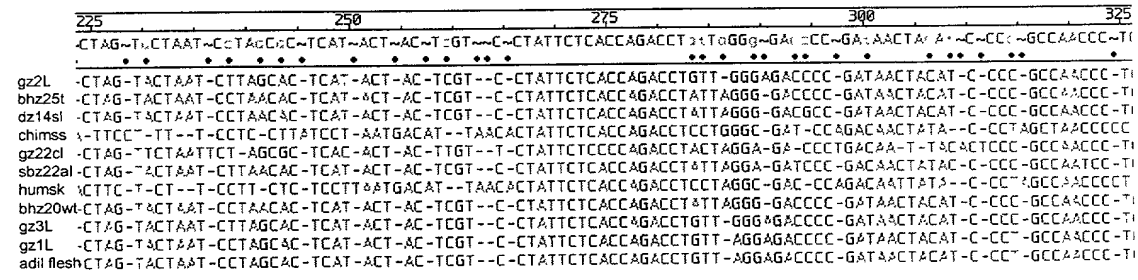


Figure 1 b

NJ-tree showing clustering of *'adil.flesh'* with 'gz1L' i.e.the known normal leopard (*Penthera pardus*)

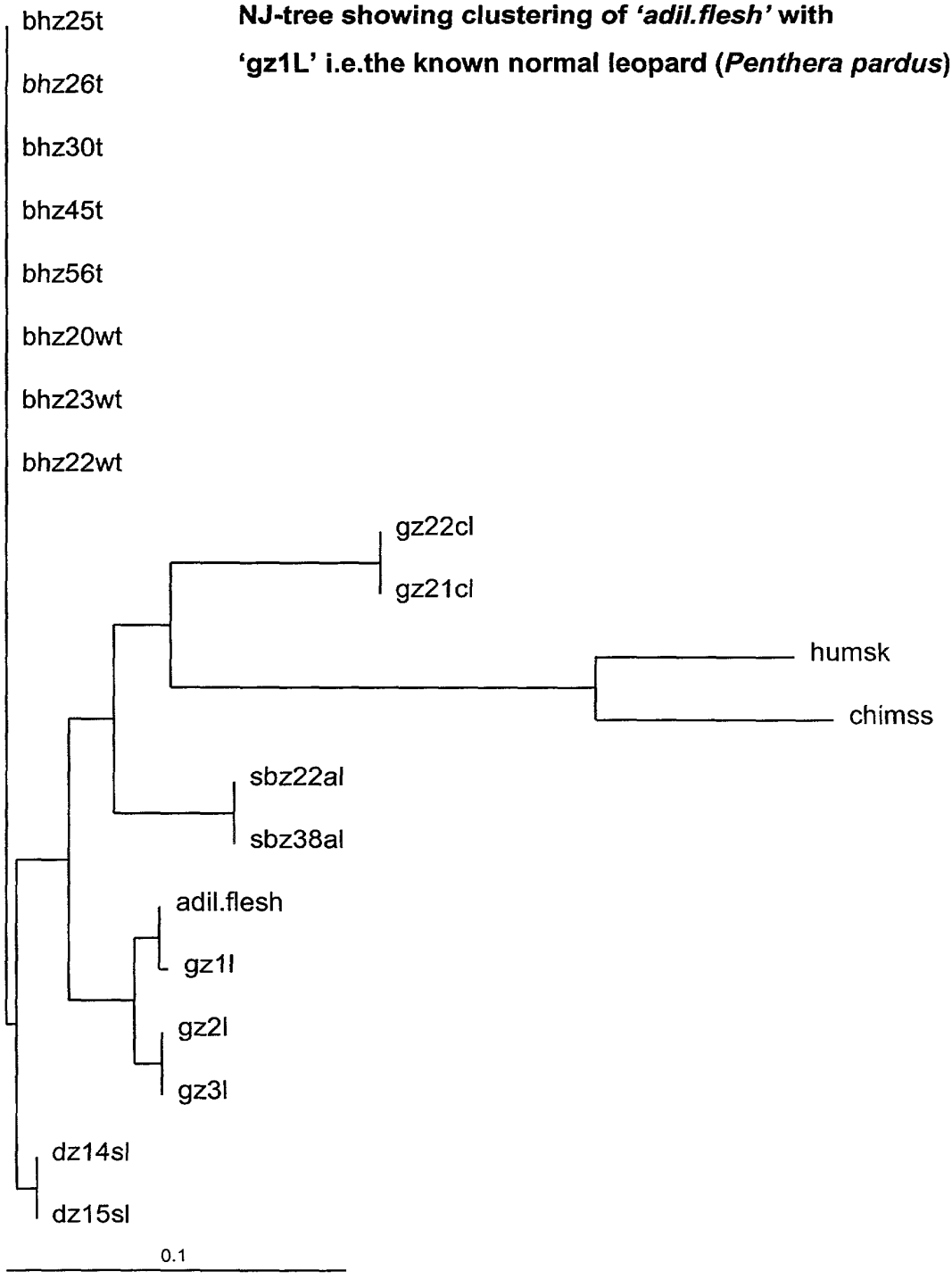


Figure 1c

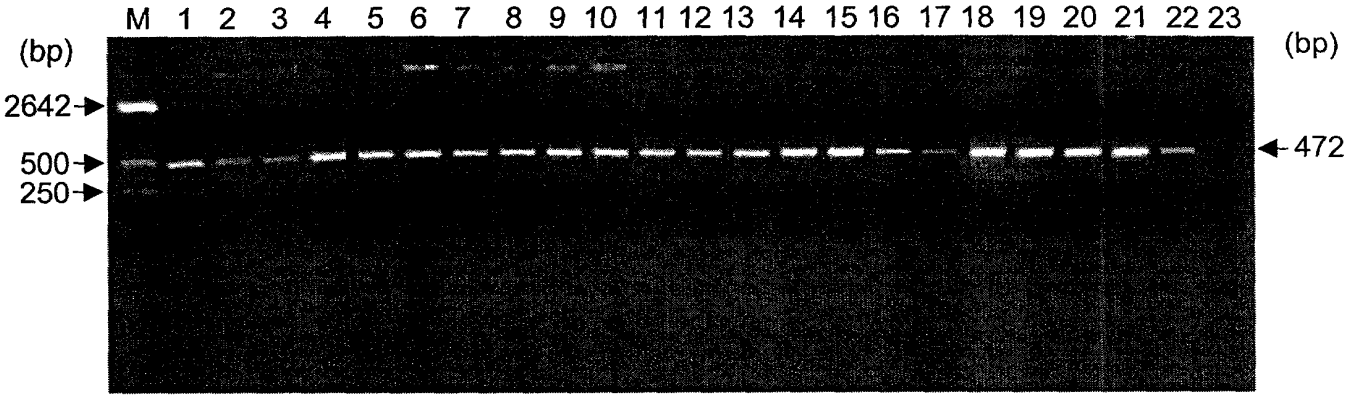


Figure 2

Replacement Sheet

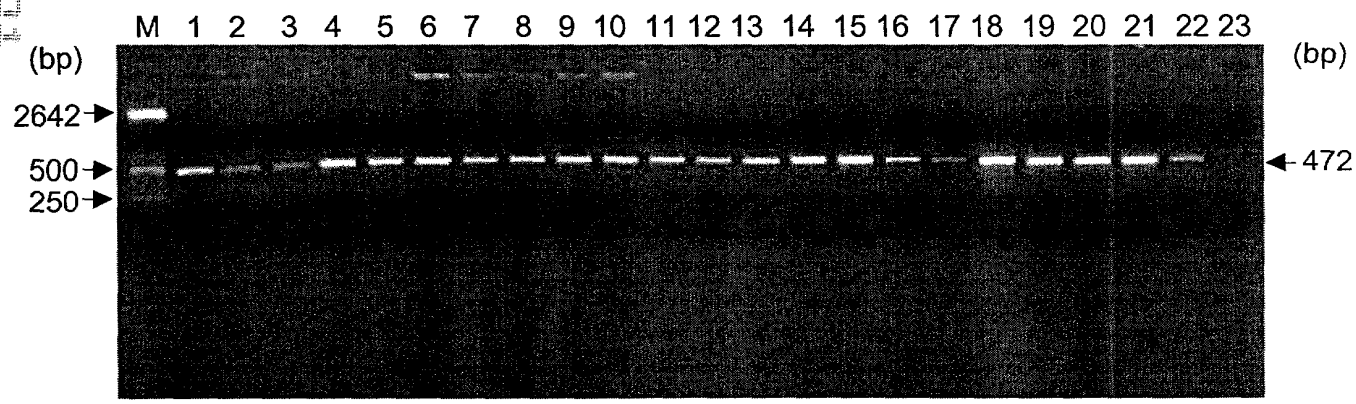


Figure 2

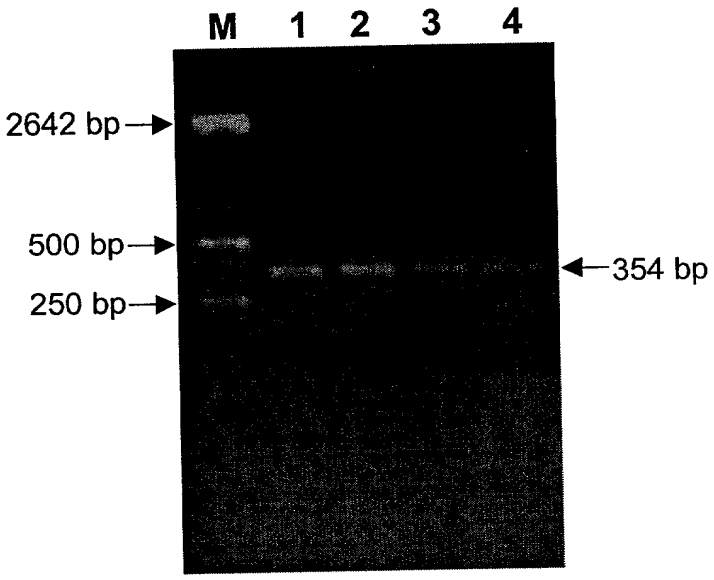


Figure 3

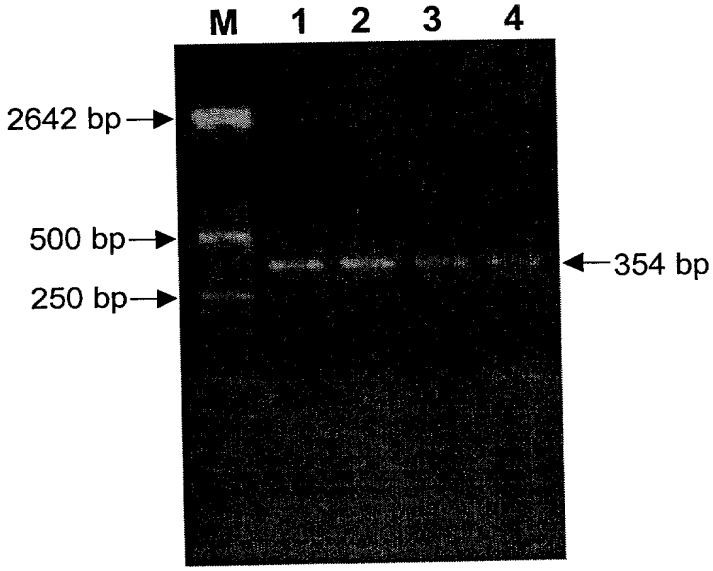


Figure 3

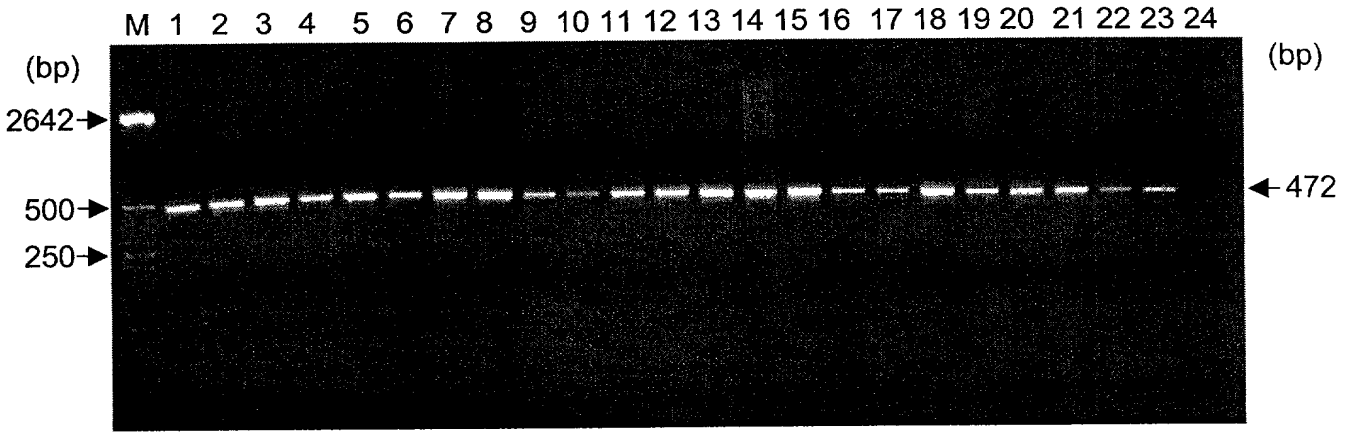


Figure 4

Replacement Sheet

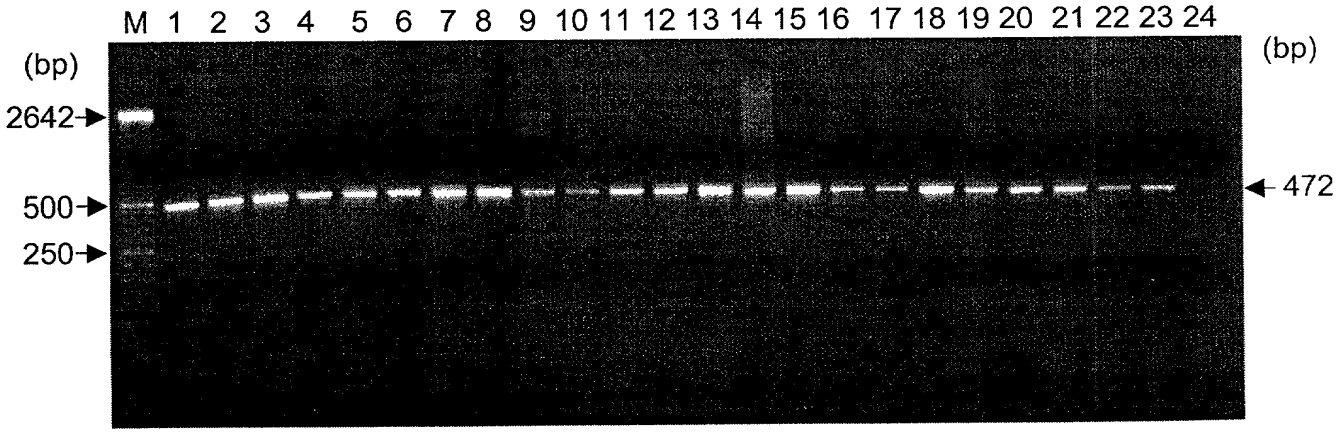


Figure 4